Prevalence of Negative Strain Gram Bacteria Extended Spectrum Beta Lactamase (ESBL) in Rsud Prof. Dr. W.Z. Johannes Kupang2016 at 2018

By NI Made Susilawati

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ORIGINAL ARTICLE

Prevalence of Negative Strain Gram Bacteria Extended Spectrum Beta Lactamase (ESBL) in Rsud Prof. Dr. W.Z. Johannes Kupang 2016 at 2018

[1]NI MADE SUSILAWATI, [2]NORMA TIKU KAMBUNO, M.KES[3],· YUDIANA INTI SAPUTRI, AMD.KES,S.SI[4], I GEDE PUTU ARNAWA, S.ST., M.SI
[1,2,3]*Department of Health Analyst, Kupang Health Polytechnic*
[4] *Department of Sanitasi, Kupang Health Polytechnic*
Correspondence to Ni Made Susilawati

ABSTRACT

Background: Antibiotics are a group of compounds that can inhibit bacterial growth (bacteriostatic) or cause of death bacterial (bactericidal). Bacterial resistance occurs due to inappropriate administration of antibiotic doses and mis of diagnosis by health workers. Bacteria that are resistant to penicillin, cephalosforin and aztreonam generally have an enzyme released to defend themselves, this enzyme is called Extended Spectrum Beta Lactamase (ESBL).
Method: This study aims to determine the number of gram-negative bacteria that produce Extended Spectrum Beta Lactamase (ESBL) which is examined from samples that are cultured in the microbiology section in the laboratory of RSUD Prof.DR.W.Z. Johannes Kupang from 2016 to 2018. Secondary data were taken, processed and presented in descriptive form.
Result::The Bacteria Extended Spectrum Beta Lactamase (ESBL) was the most found is 104 (50.9%) Klebsiella pneumoniae bacteria, followed by 56 (29.78%) Escherichia coli bacteria, and Enterobacteriaceae (3.61%). ESBL group bacteria mostly came from the Neonatal Intensive Care Unit (NICU) room as many as 26, ESBL group bacteria were mostly found in pus samples as many as 33 (19.41%).
Keywords: Extended Spectrum Beta Lactamase (ESBL), RSUD Prof.DR.W.Z. Johannes Kupang

INTRODUCTION

Antibiotics work through four main mechanisms, namely by influencing cell walls, disrupting cell membrane function, inhibiting protein synthesis and inhibiting nucleic acid synthesis[18].

These bacteria have the defense power to avoid antibiotics by mutating the active side, forming trans membrane proteins (protein efflux) and encoding plasmid genes that are resistant for antibiotics[8].

Clinically, the hydrolysis of beta lactamase antibiotics is the most frequent mechanism underlying the occurrence of resistance to beta lactam antibiotics in gram negative bacteria[3].

The beta lactamase enzyme was first identified in the Escherichia coli bacterium which was given the name ESBL type TEM or TEM. Later exploration proved that TEM was encoded by an gene resistant for antibiotic which located in the plasmid. Besides Escherichia coli, TEM enzymes are also currently found in *Pseudomonas aeruginosa,* Haemophilus influenzae and Neisseria gonorrhoeae[14].

Therapy of bacterial infection that produces beta lactamase has been using cephalosporin and aztreonam antibiotics which are also included as a beta lactam antibiotic group [4]. In fact, this drug cannot kill of bacteria, because the bacteria can develop resistance spectrum until imun to penicillin, cephalosporin and aztreonam so that this enzyme is called Extended Spectrum Beta Lactamase (ESBL)[18]. The ability of ESBL strain bacteria to hydrolyze beta lactam antibiotics is widely caused by a number of mutations in the TEM and SHV genes [5,6,7]. These mutations generally affect the active site area of the enzyme so that the activity of the enzyme increases[14,2].

Various Gram-negative bacteria, especially the family Enterobacteriaceae, including causes of nosocomial infections or known as Healthcare-Associated Infection (HAIs). In Indonesia, the incidence of HAIs is quite high at 6-16% with an average of 9.8% in 2010[9].

Several studies in America and Europe show that the prevalence of ESBL-producing bacteria reaches 60% of the existing clinical isolation [13]. So that treatment and selection of antibiotics becomes very difficult if there is a new type that is resistant to ESBL[13].

In Indonesia the prevalence of infection by ESBL-producing bacteria reaches 65%[9]. In Prof. Hospital DR. W. Z. Johannes Kupang, East Nusa Tenggara Province has not measured the number of gram-negative bacteria that produce ESBL even though paramedics has carried out the examination of bacterial culture, resistance and sensitivity to antibiotics in clinical microbiological specimens. From the description above encourages the author to conduct research on the Prevalence of Negative Gram Bacteria Strain Extended Spectrum Beta Lactamase (ESBL) in Prof. DR. Hospital. W. Z. Johannes Kupang from 2016-2018

The results of this study can be used as a reference for therapy as well as data to monitor germ resistance and sensitivity patterns, as well as to look for sources of infection if there are outbreaks in hospitals.

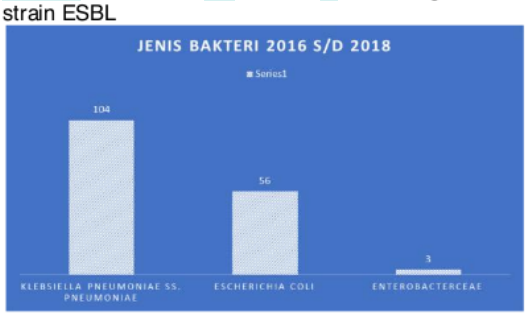
METHOD

This research was conducted by taking and processing secondary data at the Clinical Microbiology Laboratory at Prof. DR. W.Z. Johannes Kupang about the number of Gram negative bacteria ESBL strains from 2016 to 2018 from taken cultures of various specimens

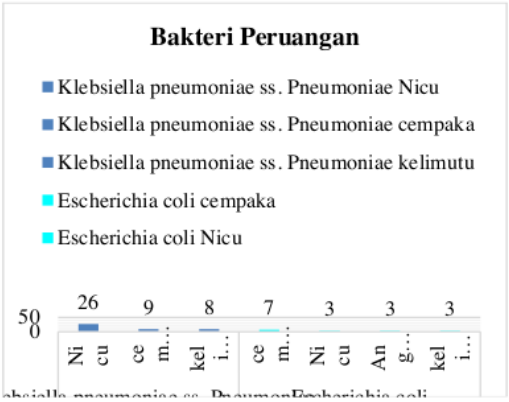
RESULTS AND DISCUSSION

Secondary data on the number of ESBL bacteria in 2016 - 2018 can be seen in table 1 below.

Table .1 Bar chart of the number of Gram-negative bacteria strain ESBL



In the chart above shows that most ESBL-producing bacteria in 2016 to 2018 were Klebsiella pneumoniae with a total sample of 204 with a total positive ESBL of 104 (50.9%), followed by Escherichia coli with a total sample of 188 with a total positive of ESBL 56 (29.78%), and Enterobacteriaceae bacteria with a total sample of 83 samples with a total positive ESBL of 3 (3.61%). So the total ESBL positive is 163. Table 2 Bar chart of the number of ESBL bacteria by room / location in 2016 – 2018



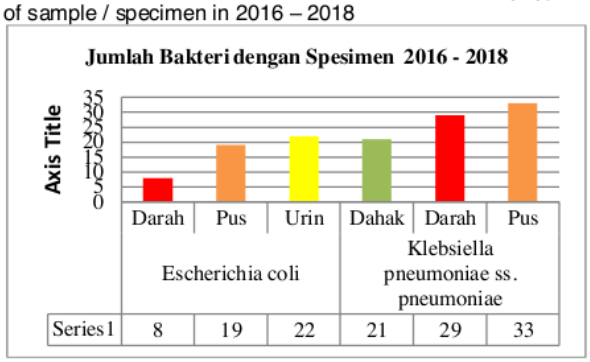
From the diagram above it can be seen that the Gram-negative bacterial strain ESBL for the room / location is most commonly found in the Neonatal Intensive Care Unit (NICU) room with the bacteria Klebsiella pneumoniae (26), and followed in room 3 for Female / Cempaka (9), then in room 3 male / Kelimutu (8). Escherichia coli was found mostly in room 3 Female / Cempaka (7), then in the Neonatal Intensive Care Unit (NICU) room (3) and room 2 Female / orchids (3) and room 3 men / Kelimutu with total bacteria (3) . Of the total bacteria, this is not included in the total than the Enterobacteriaceae bacteria because the total number is very small and is not present in one location / room.

With the discovery of the Gram-negative bacteria Enterobacteriaceae family especially in the NICU room, this is the same as previous research that Gram-negative bacteria, especially the Enterobacteriaceae family are the main bacteria that cause nosocomial infections or what is now known as Healthcare-Associated Infection (HAIs)[15]. The cause of HAIs often occurs especially in infants receiving treatment at the NICU[1]. With the discovery of Klebsiella pneumoniae in the NICU ward / ward, this is the same as the previous research that found that one bacterial Klebsiella sp. ESBL was positive at RSUD Prof.DR.W.Z.Johannes Kupang in the NICU room [10].

Bacterial resistance to antibiotics is increasingly widespread if the use is not done rationally, such as the use of antibiotics without regard to bacterial sensitivity testing[15,12].

Sources of transmission of infections that often occur in the NICU space include the use of assistive devices such as ventilators, infusions, intravenous catheters and urine catheters. Transmission can also occur directly from individuals and transmission from paramedics[16,11].

Table 3 Bar chart of the number of ESBL bacteria by type of sample / specimen in 2016 – 2018



From the diagram above it can be seen that the ESBL-producing bacteria 2016 -2018 with a total positive ESBL of 152. For the bacteria Klebsiella pneumoniae were most commonly found in pus specimens with a total positive ESBL of 33 (19.41%), in blood specimens in obtained positive ESBL of 29 (17%) and at least found in sputum samples / specimens with a total positive ESBL of 21 (12.35%). As for the Esherichia coli bacteria, the most in urine specimens with a total positive ESBL were 22 (16.66%), and the pus specimens with a total positive ESBL were 19 (14.39%) and the least was found in blood samples with a total positive ESBL. as many as 8 (4.70%). While the rest for positive ESBL bacteria as many as 10 (5.88%) were found in different samples / specimens with different types of bacteria as well as in Enterobacteriaceae (2) in pus specimens, Enterobacter cloacae (1) in pus specimens, Providencia stuartii (1), in urine specimens, Klebsiella oxytoca (3) in pus specimens, Pseudomonas aeruginosa (1) in pus specimens and Proteus sp (2) in pus specimens.

CONCLUSION

The most isolated types of ESBL 2016-2018 were Klebsiella pneumonia with percentage (50.9%), Escherichia coli (29.78%), and Enterobacteriaceae (3.61%),

Most room/location for the type of bacteria Klebsiella pneumoniae were found in the Neonatal Intensive Care

Unit (NICU) room (26), then followed by room 3 Female / Cempaka[9] and in room 3 Male / Kelimutu[8]. In Escherichia coli bacteria, it is found mostly in room 3 for Female / Cempaka[7], in the Neonatal Intensive Care Unit (NICU) room[3] then in room for 2 Female / Orchid), room 3 for Male / Kelimutu[3] .

The most samples for the type of bacteria Klebsiella pneumoniae with a positive ESBL percentage of 33(19.41%), were found in pus specimens, in blood specimens there were positive ESBLs of 29(17%) and the least were found in sputum / sputum specimens / specimens with a total positive ESBL of 21(12.35%). As for the Esherichia coli bacteria, most were in urine specimens with a total positive ESBL of 22(16.66%), and in pus specimens with a total positive ESBL as many as 19 (14.39%) and the least were found in blood samples with a total positive ESBL as many as 8 (4.70%). While the remaining 10 positive ESBL bacteria were found (5.88%) in different samples / specimens with different types of bacteria.

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